Raw Sequence Listing Error Summary

#4

ERROR DETECTED   **SUGGESTED CORRECTION**

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES) — Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

This Raw Listing contains the General Information
Section and up to first 5 pages.   Does Not Comply
                                    Corrected Diskette Needed

1	<110> APPLICANT: Borriello, Francescopaolo	
2	Band, Hamid	
3	<120> TITLE OF INVENTION: Characterization of a novel gene Cbl-SL	
4	<130> FILE REFERENCE: B0801/7159/ERP	
5	<140> CURRENT APPLICATION NUMBER: US/09/434,708	
6	<141> CURRENT FILING DATE: 1999-11-05	
7	<150> EARLIER APPLICATION NUMBER: U.S. 60/107,470	
8	<151> EARLIER FILING DATE: 1998-11-06	
9	<160> NUMBER OF SEQ ID NOS: 10	
10	<170> SOFTWARE: FastSEQ for Windows Version 3.0	
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21	1 5 10	
22	gag gcc cgc gcc ctg ggc cgg gca gtc agg atg ctg cag cgc cta gaa	99
23	Glu Ala Arg Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu	
24	15 20 25	
25	gag caa tgc gtc gac ccc cgg ctg tcc gtg agt ccc cct tcg ctg cgg	147
26	Glu Gln Cys Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg	
27	30 35 40 45	
28	gac ctg ctg ccc cgc aca gcg cag ctg ctt cga gag gtg gcc cat tct	195
29	Asp Leu Leu Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser	
30	50 55 60	
31	cgg cgg gcg gcc ggc gga ggc ggc ccc ggg ggt ccc ggc ggc tct ggg	243
32	Arg Arg Ala Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly	
33	65 70 75	
34	gac ttt cta ctc atc tac ctg gcc aat ctg gag gcc aag agc agg cag	291
35	Asp Phe Leu Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln	
36	80 85 90	
37	gtg gcc gcg ctg ctg cct ccc cgg ggc cga agg agt gcc aac gac gag	339
38	Val Ala Ala Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu	
39	95 100 105	
40	ctc ttc cgg gcg ggc tcc aga ctc agg cga cag ctg gcc aag ctg gcc	387
41	Leu Phe Arg Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala	
42	110 115 120 125	
43	atc atc ttc agc cac atg cac gca gag ctg cac gca ctc ttc ccc ggg	435
44	Ile Ile Phe Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly	

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45                    130              135              140
46    gca aag tac tgt gga cac atg tac cag ctc acc aag gcc ccc gcc cac    483
47    Ala Lys Tyr Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His
48                    145              150              155
49    acc ttc tgg agg gaa agt tgc gga gcc cgg tgt gtg ctg ccc tgg gct    531
50    Thr Phe Trp Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala
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52    gag ttt gag tcc ctc ctg ggc acc tgc cac cct gtg gaa cca ggc tgc    579
53    Glu Phe Glu Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys
54              175              180              185
55    aca gcc ctg gcc ttg cgc acc acc att gac ctc acc tgc agc ggg cac    627
56    Thr Ala Leu Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His
57    190              195              200              205
58    gtg tcc atc ttc gag ttc gac gtc ttc acc agg ctc ttt cag cca tgg    675
59    Val Ser Ile Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp
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61    cca aca ctc ctc aag aac tgg cag ctc ctg gca gtc aac cac cca ggc    723
62    Pro Thr Leu Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly
63                    225              230              235
64    tac atg gcc ttc ctc acc tat gat gag gtc caa gag cgt ctg cag gcc    771
65    Tyr Met Ala Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala
66                    240              245              250
67    tgc agg gac aag cca ggc agt tac atc ttc cgg ccc agc tgt act cgc    819
68    Cys Arg Asp Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg
69              255              260              265
70    ctg ggg cag tgg gcc atc ggc tat gtg agc tca gat ggc agc atc ctg    867
71    Leu Gly Gln Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu
72    270              275              280              285
73    cag acc atc cct gcc aac aaa ccc ctg tcc cag gtg ctc ctg gag gga    915
74    Gln Thr Ile Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly
75                    290              295              300
76    cag aag gac ggc ttc tac ctc tac cca gat gga aag acc cac aac cca    963
77    Gln Lys Asp Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro
78                    305              310              315
79    gac ctg act gag ctc ggc cag gca gaa ccc cag cag cgc atc cac gtg    1011
80    Asp Leu Thr Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val
81              320              325              330
82    tca gag gag cag ctg cag ctc tac tgg gcc atg gac tcc aca ttt gag    1059
83    Ser Glu Glu Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu
84              335              340              345
85    ctc tgc aag atc tgt gct gag agc aac aag gat gtg aag att gag ccg    1107
86    Leu Cys Lys Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro
87    350              355              360              365
88    tgc ggg cac ctg ctc tgc agc tgc tgc ctg gct gcc tgg cag cac tcg    1155
89    Cys Gly His Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser
90                    370              375              380
91    gac agc cag acc tgc ccc ttc tgc cgc tgc gag atc aag ggc tgg gag    1203
92    Asp Ser Gln Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu
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94    gcc gtg agt atc tac cag ttc cac ggt cag gct act gct gag gac tca    1251
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 97        ggg aac agc agt gac cag gaa ggc agg gag ttg gag ctg ggg cag gtg        1299
 98        Gly Asn Ser Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val
 99                    415                 420                 425
100        ccc ctt tcg gct cct cca ttg ccc cca cgg cca gat ctg ccc ccc agg        1347
101        Pro Leu Ser Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg
102                    430                 435                 440             445
103        aag ccc aga aat gcc cag ccg aaa gtg aga ctc cta aag ggg aac tcc        1395
104        Lys Pro Arg Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser
105                    450                 455                 460
106        cct cca gct gcg ctg gga ccc cag gac cct gcc ccg gcc tgaaggccag         1444
107        Pro Pro Ala Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala
108                    465                 470
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119                     20                  25                  30
120        Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg Asp Leu Leu
121                     35                  40                  45
122        Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala
123                  50                  55                  60
124        Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly Asp Phe Leu
125         65                  70                  75                  80
126        Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala
127                     85                  90                  95
128        Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg
129                    100                 105                 110
130        Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe
131                    115                 120                 125
132        Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Ala Lys Tyr
133                    130                 135                 140
134        Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp
135         145                 150                 155                 160
136        Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu
137                    165                 170                 175
138        Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu
139                    180                 185                 190
140        Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile
141                    195                 200                 205
142        Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu
143                    210                 215                 220
144        Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly Tyr Met Ala
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145          225                  230                  235                  240
146      Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg Asp
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148      Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu Gly Gln
149                       260                  265                  270
150      Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu Gln Thr Ile
151                  275                  280                  285
152      Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly Gln Lys Asp
153          290                  295                  300
154      Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro Asp Leu Thr
155      305                  310                . 315                  320
156      Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val Ser Glu Glu
157                       325                  330                  335
158      Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu Leu Cys Lys
159                  340                  345                  350
160      Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro Cys Gly His
161                  355                  360                  365
162      Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser Asp Ser Gln
163          370                  375                  380
164      Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu Ala Val Ser
165      385                  390                  395                  400
166      Ile Tyr Gln Phe His Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser
167                       405                  410                  415
168      Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser
169                  420                  425                  430
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171                  435                  440                  445
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187      ctggccaagc tggccatcat cttcagccac atgcacgcag agctgcacgc actcttcccc    420
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191      acctgcagcg gcacgtgtc catcttcgag ttcgacgtct tcaccaggct ctttcagcca    660
192      tggccaacac tcctcaagaa ctggcagctc ctggcagtca accacccagg ctacatggcc    720
193      ttcctcacct atgatgaggt ccaagagcgt ctgcaggcct gcagggacaa gccaggcagt    780
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        244          tggacccccct c                                                         491
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/434,708**

Input Set: **I434708.RAW**

Line	?	Error/Warning	Original Text
211	W	"N" or "Xaa" used: Feature required	ccttgagcag cacatctggg tgccctggcc ttcagcgg
212	W	"N" or "Xaa" used: Feature required	cgcangangn gggagttccc ctttaggagt ctcacttt
213	W	"N" or "Xaa" used: Feature required	ctggggggca gatctggccg tgggggcaat ggaggagc
216	W	"N" or "Xaa" used: Feature required	gtctgggctg tccgagtgct gccaggcanc caggcagc
223	W	"N" or "Xaa" used: Feature required	agggacaagc caggcagtta catcttccgg cccagctg
224	W	"N" or "Xaa" used: Feature required	atcgntattg tgagctcaga tggcagcatc ctgcagac
241	W	"N" or "Xaa" used: Feature required	cctggcagaa ctcagacagn ccagacctgc cctttct
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243	W	"N" or "Xaa" used: Feature required	aangacncca ngggacagc agtggccaag ggaagatg